

Claims

1. Method for analysis of a regulatory genetic network of a cell using a causal network, said causal network describing the regulatory genetic network of the cells such that nodes of the causal network represent genes of the regulatory genetic network and connectors of the causal networks represent regulatory interactions between the genes of the regulatory genetic network,
 - a) in which for a selected gene of the regulatory genetic network a gene expression rate is predetermined,
 - b) in which, by using the causal network for the predetermined gene expression rate a resulting gene expression pattern is generated for the regulatory genetic network;
 - c) in which the generated resulting gene expression pattern is compared with a predetermined gene expression pattern of the regulatory genetic network.
2. Method in accordance with claim 1,
in which the selected gene is selected using the causal network by means of a dependency analysis.
3. Method in accordance with one of the previous claims,
in which the gene expression rate of the selected gene is predetermined such that the predetermined gene expression rate of the selected gene reflects an assumption of a gene defect.
4. Method in accordance with one of the previous claims, in
which the causal network is a Bayesian network is.
5. Method in accordance with one of the previous claims,
in which the causal network is of a type DAG (directed acyclic graph).
6. Method in accordance with one of the previous claims,
in which the generated resulting and/or the predetermined gene

expression pattern represents discrete gene states.

7. Method in accordance with one of the previous claims,
-in which the represented discrete gene states are an
overexpressed, a normally expressed and an underexpressed gene
state.

8. Method in accordance with one of the previous claims,
in which the generated resulting gene expression pattern is
compared to the predetermined gene expression pattern using a
static method and/or a statistical code, especially a measure
of distance.

9. Method in accordance with one of the previous claims,
in which the causal network is trained using the gene
expression patterns, with the nodes and the connectors of the
causal networks being adapted.

10. Method in accordance with one of the previous claims,
In which the gene expression pattern, especially the
predetermined gene expression pattern and/or the gene
expression pattern for training, are determined using a DNA
microarray technique.

11. Method in accordance with one of the previous claims,
in which the predetermined gene expression pattern and/or the
gene expression pattern for the training are gene expression
patterns of a genetic regulatory network of a diseased cell.

12. Method in accordance with one of the previous claims,
in which the diseased cell is an oncocyte especially eine
oncocyte with ALL (Acute Lymphoblastic Leukemia).

13. Method in accordance with one of the previous claims,
in which the diseased cell features an oncogene, especially an
ALL oncogene.

14. Method in accordance with one of the previous claims, in which for a plurality of selected genes of the regulatory genetic network a gene expression rate is predetermined in each case, a plurality of resulting gene expression patterns are generated and a plurality of comparisons are performed.

15. Method in accordance with one of the previous claims, in which the generation the plurality of resulting gene expression patterns is performed iteratively.

16. Method in accordance with one of the previous claims, used for identification of a dominant gene.

17. Method in accordance with one of the previous claims, used for identification of a degenerated/mutated/diseased/oncogene/tumor-suppressor gene.

18. Method in accordance with one of the previous claims, used for identification of a tumor cell.

19. Method in accordance with one of the previous claims, used for cancer detection.

20. Method in accordance with one of the previous claims, used to analyze the cause of an abnormal gene expression pattern/gene expression rate.

21. Method in accordance with one of the previous claims, Used for a simulation and/or analysis of the effect of a medicament..

22. Computer program product with program code means, to execute all steps according to claim 1 when the program is executed on a computer.

23. Computer program product with program code means according

to the previous claim, said program code means being stored on a machine-readable data medium.

24. Computer program product with program means stored on a machine-readable data medium, to perform all steps according to claim 1, when the program is executed on a computer.